AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1.   (Currently amended) A method of identifying a cell, tissue or nucleus, comprising:

obtaining a DNA methylation pattern for the cell, tissue or nucleus, wherein the DNA methylation pattern for the cell, tissue, or nucleus comprises information on the methylation state of a plurality of gene regions;

obtaining a DNA methylation pattern for one or more known types of cell, tissue or nucleus, wherein the DNA methylation pattern for the one or more known types of cell, tissue or nucleus comprises information on the methylation state of a plurality of gene regions; and, after obtaining the DNA methylation patterns,

comparing the DNA methylation patterns thus obtained ~~of the cell, tissue or nucleus with the DNA methylation pattern of the one or more known types of cell, tissue or nucleus~~, thereby identifying the cell, tissue or nucleus.

2.   (Canceled)

3.   (Canceled)

4.   (Withdrawn) A computer-readable record medium in which a program that permits a computer to function as an identification system for cells, tissues or nuclei has been recorded, said identification system comprising:

(a)   means for analyzing information on the methylation pattern of DNA isolated from a test cell, tissue or nucleus; and

(b)   means for identifying the cell, tissue or nucleus using the analysis results as an indicator.

5.   (Currently amended)   A method of assessing the differentiation state of a cell, tissue or nucleus comprising:

obtaining a DNA methylation pattern for the cell, tissue or nucleus, wherein the DNA methylation pattern for the cell, tissue or nucleus comprises information on the methylation state of a plurality of gene regions;

obtaining a DNA methylation pattern for one or more cell, tissue or nucleus of known differentiation state, wherein the DNA methylation pattern for the one or more cell, tissue or nucleus of known differentiation state comprises information on the methylation state of a plurality of gene regions; and, after obtaining the DNA methylation patterns,

comparing the DNA methylation patterns thus obtained of the cell, tissue or nucleus with the DNA methylation pattern of the one or more cell, tissue or nucleus of known differentiation state, thereby assessing the differentiation state of the cell, tissue or nucleus.

6.   (Currently amended) The method of claim 5, wherein the DNA methylation patterns each comprise information on the methylation state of at least about 1,000 gene regions.

7.   (Previously presented) The method of claim 5, further comprising identifying the methylated and demethylated gene regions that specify the differentiation state of the cell, tissue, or nucleus.

8.   (Previously presented)   The method of claim 5, wherein the cell, tissue, or nucleus is a stem cell.

9.   (Previously presented)   The method of claim 5, wherein the DNA methylation patterns are analyzed by generating RLGS profiles.

10.   (Currently amended) The method of claim 1, wherein the DNA methylation patterns each comprise information on the methylation state of at least about 1,000 gene regions.

11.   (Previously presented)   The method of claim 1, further comprising identifying the methylated and demethylated gene regions that specify the identity of the cell, tissue, or nucleus.

12.   (Previously presented)   The method of claim 1, wherein the cell, tissue, or nucleus is a stem cell.

13.   (Previously presented)   The method of claim 1, wherein the DNA methylation patterns are analyzed by generating RLGS profiles.

14.   (Withdrawn) A method of producing a differentiated cell, tissue, or nucleus comprising:

methylating or demethylating the gene regions identified by the method of claim 7

in a cell, tissue, or nucleus, so as to specify a desired differentiation state; and

producing a differentiated cell, tissue, or nucleus.